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ANALYSIS OF A PUTATIVE AUTOPHAGY REGULATOR DURING STRAWBERRY FRUIT RIPENING

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Autophagy is a major catabolic pathway essential for cell homeostasis and conserved in almost all eukaryotes. During autophagy, cytoplasmic components are engulfed by a double membrane vesicle called autophagosome and transported to the vacuole were its content it is degraded by lytic enzymes (Marshall and Vierstra, 2018). Autophagy is important in many developmental processes and in response to both biotic and abiotic stresses (Lv, 2014). Recently, we have determined that autophagy is active during strawberry fruit ripening and that it has an essential role for the proper progression of this developmental process (Sánchez-Sevilla, 2021). In this work we have focused on the study of the role of a transcription factor as putative regulator of autophagy during strawberry ripening. We have analyzed its expression during strawberry ripening is in different *FxaATG* genes and analyzed the interaction between this transcription factor with three different autophagy related genes by a luciferase assay performed in Nicotiana benthamiana leaves.

References:

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